

WHAT IS CLAIMED IS:

1. A method of nucleic acid sequencing comprising the steps:

5 (a) amplifying a nucleic acid sample to produce an amplified DNA product;

(b) extending a sequencing primer bound to the DNA product in the presence of terminating nucleotide analogs to
10 produce a collection of labeled nucleic acid products;

(c) detecting a total amount of label present in the collection to produce a measurement; and

(d) combining a plurality of measurements to determine DNA sequence information about the sample.

2. A method as described in Claim 1 wherein each measurement of a label corresponds to an amount of terminating nucleotide.

3. A method as described in Claim 1 wherein the DNA sequence information corresponds to a length of the DNA sequence.

4. A method as described in Claim 1 wherein the DNA sequence
25 information corresponds to a plurality of bases in the DNA sequence.

5. A method as described in Claim 1, wherein after the combining step, the DNA sequence information is used for human
30 identification.

6. A method as described in Claim 1, wherein after the combining step, the DNA sequence information is used for diagnostic testing.

7. A method as described in Claim 1, wherein after the combining step, the DNA sequence information is used for genetic localization or gene discovery.

5 8. A method as described in Claim 1, wherein after the combining step, the DNA sequence information is used for criminal justice applications.

10 9. A method as described in Claim 1, wherein after the combining step, the DNA sequence information is used in conjunction with a DNA database of genetic polymorphisms.

15 10. A method as described in Claim 1, wherein after the combining step, the DNA sequence information is used for cancer assessment.

11. A system for nucleic acid sequencing comprising:

20 (a) a means for amplifying a nucleic acid sample to produce an amplified nucleic acid product;

25 (b) a means for extending a sequencing primer bound to the DNA product in the presence of terminating nucleotide analogs to produce a collection of labeled nucleic acid products, said extending means in connection with the amplified product;

(c) a means for detecting a total amount of label present in the collection to produce a measurement, said detecting means in connection with the collection; and

30 (d) a means for combining a plurality of measurements to determine DNA sequence information about the sample, said combining means in connection with the measurement.

12. A system as described in Claim 11, wherein the amplifying means includes a PCR thermocycler, the extending means includes a chamber that permits DNA sequencing reactions to occur in the presence of terminating nucleotide analogs, the detecting means
5 measures fluorescent or other labels that quantify an amount of DNA molecules, and the combining means includes a computing device with memory.

13. A method for obtaining information about a signal comprising
10 the steps:

(a) inducing a decay function;

(b) imposing the decay function on a signal;

(c) forming a numerical quantity that characterizes the signal's behavior in the presence of the decay function;

(d) combining a plurality of such numerical quantities to
20 obtain information about the signal.

14. A method as described in Claim 13 wherein the signal is a nucleic acid sequence, the decay function is induced by introducing dideoxy terminator analogs into a sequencing reaction,
25 the numerical quantities correspond to Laplace transform coefficients, and the obtained information helps characterize the sequence.

15. A method as described in Claim 14 wherein the characterization
30 does not completely describe the nucleic acid sequence.

16. A method as described in Claim 15 wherein the incomplete sequence information describes a genetic polymorphism.